

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: April 13, 2003, 02:11:28 ; Search time 129.415 seconds
(without alignments)
3373.191 Million cell updates/sec

Title: US-09-813-990A-1_COPY_441_455

Perfect score: 15

Sequence: 1 ggttgcttttctact 15

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBank:

- 1: gb_ba.*
- 2: gb_hgt.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vt.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vt.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_inv.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rtd.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	2193	1	PI044367
2	15	100.0	4992	3	AB048261
3	15	100.0	5263	1	FL058
4	15	100.0	20915	1	AB006946
5	15	100.0	27030	1	M101237
6	15	100.0	85341	2	AC115302
7	15	100.0	101075	8	AC006430
8	15	100.0	103324	2	AC126433
9	15	100.0	138225	2	AC125755
10	15	100.0	153363	2	AC127395
11	15	100.0	165509	2	AC069886
12	15	100.0	167457	2	AC112446
13	15	100.0	157640	2	AC128090
14	15	100.0	158634	9	AL357472
15	15	100.0	172511	2	AC126462
16	15	100.0	172589	2	AC115562
17	15	100.0	176713	9	AP000751
18	15	100.0	176942	9	AC357420
19	15	100.0	186832	2	AC125319
20	15	100.0	189747	2	AC087231
21	15	100.0	190131	2	AC122368
22	15	100.0	192313	2	AF031265
23	15	100.0	199806	2	AC025360
24	15	100.0	213888	2	AC122506
25	15	100.0	225143	2	AC122263
26	15	100.0	231668	2	AC058861
27	15	100.0	241392	2	AC119239
28	15	100.0	245163	2	AL162453
29	14	93.3	780	6	AX414043
30	14	93.3	790	6	AX415217
31	14	93.3	841	9	HS034151
32	14	93.3	895	4	AF165618
33	14	93.3	935	5	AF065709
34	14	93.3	1552	9	AF052392
35	14	93.3	1618	4	AF035405
36	14	93.3	1849	4	HS000407
37	14	93.3	2045	8	AF033138
38	14	93.3	2097	8	AF051134
39	14	93.3	3339	9	H0050702
40	14	93.3	3772	9	HS055306
41	14	93.3	5495	10	M053580
42	14	93.3	6693	5	HC033875
43	14	93.3	8000	1	AF068902
44	14	93.3	8000	6	AX192753
45	14	93.3	10029	1	AF058439

ALIGNMENTS

RESULT 1
E044367
LOCUS
DEFINITION
Phlebotomus leishmanosarum B71.1172153
gene, partial cds.
ACCESSION
044367
KEYWORDS
SOURCE
ORGANISM
Phlebotomus leishmanosarum B71.1172153
Phlebotomus leishmanosarum B71.1172153
Bacterial: Proteobacteria; alpha subdivision; Phlebotominae group;
Phlebotominae; Phlebotomus.
REFERENCE
1 (bases 1 to 2193)
AUTHORS
Krol, J. and Skorupska, A.
TITLE
Identification of genes in Phlebotomus leishmanosarum B71.1172153

1 GGTTCGTTCTGCT 15
|||||
403 GGTTCGTTCTGCT 389

RESULT 3

LOCUS
Rhizobium leguminosarum prsD, prsE, ORF3 genes.
X98117
X98117.1 GI:1806273
ORF3 gene; prsD gene; prsE gene.
Rhizobium leguminosarum.
Rhizobium leguminosarum.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
1 (bases 1 to 5263)
Krol, J. and Skorupska, A.
Identification of genes in Rhizobium leguminosarum bv. trifolii
whose products are homologues to a family of ATP-binding proteins
Microbiology 143 (Pt 4), 1389-1394 (1997)
97286554
9141701
2 (bases 1 to 4423)
Krol, J. E.
Direct Submission
Submitted (24-MAY-1996) J. E. Krol, Maria Curie Sklodowska
University - Lublin, Dept. of General Microbiology, Akademicka 19,
PL- 20 033 Lublin, POLAND
On Jan 29, 1997 this sequence version replaced gi:1360123.
Location/Qualifiers
1. 5263
/organism="Rhizobium leguminosarum"
/strain="TAI"
/sub_species="trifolii"
/db_xref="taxon:384"
/clone="PARF136"
/sub_clone="PJEL"
/clone_lib="PARF136"
1250..1254
1256..1268
/gene="prsD"
1256..1268
/gene="prsD"
/codon_start=1
/trans_table=11
/protein_id="CA66799.1"
/db_xref="GI:1360124"
/db_xref="SPTREMBL:Q57040"
/translation="MQGLVFGTASALINILYLSFPMLEVDVTPSKSPISLAV
LAILALMLVCFQAEVLRSLRVAGALDEWNGRVFRALIKAPLVKXIGGGLQ
LRDQIRLFLSGMPTAMFDPWLPFYIVICFLPFAIGYIAIGGSVLAILTFIN
QGTRTSKKSSANRNFAQTIRNSEVHAMAGTMAEWDKRNSEYRIITRO
SDVNGVATLKFIRIALQSGTLATGILVIOGASSGIIAGSLTSLAPVRAAI
VSPCLAGSALVIGYSAGSKSLARMGWTPVRSIRDLGALQWGDALGRI
GYLPQDVELFSGTACNCRFAKMSPEVVAARAARHDLILPUNGETEIGEG
AALSAGORALALRALGEPFLVLDPEPNSLDEGERALSAIMSVRAGGVVVI
AHRSGVLAVCDVLMQEGRMATFGPKPEEVLARVSRPEAATPTIAERVAQLKVVVDGM
NAAE"
2975..2981
2984..4285
/gene="prsE"
2984..4285
/gene="prsE"
/codon_start=1
/trans_table=11
/protein_id="CA66800.1"
/db_xref="GI:1360125"
/db_xref="SPTREMBL:Q52859"
/translation="MSKVISESKSLNRHVAVGVLSIALVCGIGGMAAT-ELSSAVI
GEGVIVDPKCONIHLTGIVSELYSENDHVTAGOVILRLDGTTPANLSIVESTL
AQLVARRARLKAERIGAESFEVEENITDLISSAQKLLDGEQKJFDSRRSALIGMKS

RBS

gene

CDS

GAARKKQALAEIKGKQVWVAININSLSEIEFEKSSDVLYKKQCVILHPSAKAGT
RSPQKQNGSKSGEGKAIIDRQICIDDEFESEIAKIDNAGAHAEHAEHAE
KSTISQTSINPAARSSAPVHVWVTDROQLMIVVHNNELVAVKATRQIE
VHVQSVNRAEAFATPITDVSQDELISAPETVKQKETSISYRPAVHPPESTIAK
KTKLYPQDAEVEIKQIEIVSYLKEIQEQMCHVEQE
4422..4426
4433..4482
/gene="ORF3"
4433..4482
/gene="ORF3"
/codon_start=1
/trans_table=11
/protein_id="CA66801.1"
/db_xref="GI:1360274"
/db_xref="SPTREMBL:Q52900"
/translation="MICALMEAAAEPRKPAQIVLFLACINVLNATNAGVAFPII
KIVAGSILVARGWQPAETELAAELRPAKVSVAKSGETISAKLITDTRVAREQ
DILLIYANAIADHPFVSAKRSKSEIILNLEQETCAPLESP"
BASE COUNT 1123 a 1430 c 1553 g 1259 t

Query Match

Best Local Similarity 100.0% Score 150 DP 11 Length 5263
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Q7 1 GGTTCGTTCTGCT 15

|||||
25 2036 GGTTCGTTCTGCT 210

RESULT 4

AF006946

LOCUS

DEFINITION

complete genome

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

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AUTHORS

BASE COUNT 11 a 17 c 9 g 14 t
ORIGIN

Query Match 100.0%; Score 11; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTGCTCCCG 11
|||||
DB 1 TTCTGCTCCCG 11

RESULT 6
AR122817/c
LOCUS AR122817 71 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 39 from patent US 6168778.
ACCESSION AR122817
VERSION AR122817.1 GI:14107783
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 71)
AUTHORS Janjic,N., Gold,L., Schmidt,P. and Vargese,C.
TITLE Vascular endothelial growth factor (VEGF) Nucleic Acid Ligand
Complexes
JOURNAL Patent: US 6168778-A 39 02-JAN-2001;
FEATURES
Location/Qualifiers
source
1..71
/organism="unknown"

BASE COUNT 19 a 18 c 26 g 8 t
ORIGIN

Query Match 100.0%; Score 11; DB 6; Length 71;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTGCTCCCG 11
|||||
DB 23 TTCTGCTCCCG 13

RESULT 7
AX368155/c
LOCUS AX368155 144 bp DNA linear PAT 16-FEB-2002
DEFINITION Sequence 865 from Patent WO020454.
ACCESSION AX368155
VERSION AX368155.1 GI:18856228
KEYWORDS
SOURCE human.
ORGANISM human.
REFERENCE 1
AUTHORS Wang,T., Watanabe,Y., Henderson,R.A., Johnson,J.C., Retter,M.W.,
Marnerakis,M., Carter,D., Fanger,G.R., Vedvick,T.S., Bangui,C.S.,
McNabb,A., Fanger,N., Switzer,A., McNeill,P.D. and Clapper,J.C.,
TITLE Compositions and methods for the therapy and diagnosis of lung
cancer
JOURNAL Patent: WO 020454-A 865 17-JAN-2002;
CORIXA CORPORATION (US)
FEATURES
Location/Qualifiers
source
1..144
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 23 a 50 c 37 g 34 t
ORIGIN

Query Match 100.0%; Score 11; DB 6; Length 144;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTGCTCCCG 11

DB 132 TTCTGCTCCCG 128

RESULT 8
HS88A6F

LOCUS HS88A6F 160 bp DNA linear PRI 22-OCT-1995
DEFINITION H.sapiens CpG island DNA genomic MseI fragment, clone 88a6, forward
read cp988a6.r11a.

ACCESSION 263622
VERSION 263622.1 GI:103600
KEYWORDS CpG island; genomic MseI fragment.
SOURCE Homo sapiens.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 160)
AUTHORS Macdonald,M., Hocke,E., Wilkins,P. and Micklem,G.
TITLE Direct Submission
JOURNAL Submitted (16-OCT-1995) The Sanger Centre, Hinxton, Cambridgeshire,
CB10 1HQ, England. E-mail contact: hmquerry@sanger.ac.uk
REFERENCE 2 (bases 1 to 160)
AUTHORS Cross,S.H., Charlton,J.A., Nau,X. and Bird,A.P.
TITLE Purification of CpG islands using a methylated DNA binding column
METH. ENZ. 242:207-217 (1998)
JOURNAL Nat. Genet. 5 (3): 236-241 (1994)
FEATURES
Vector: pGEM-521(-)
Clones are available from the UK MRC Human Genome Mapping Project
Resource Centre, Hinxton, Cambridgeshire CB10 1HQ, UK. See URL:
http://www.hgmp.mrc.ac.uk/ for details
or contact: hickelp@hmp.mrc.ac.uk.
Location/Qualifiers
1..160
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="88a6"
/sex="male"
/tissue_type="Blood"
/clone_lib="CGI-1"
/dev_stage="adult"

BASE COUNT 17 a 57 c 46 g 32 t 6 others
ORIGIN

Query Match 100.0%; Score 11; DB 9; Length 160;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTGCTCCCG 11
|||||
DB 89 TTCTGCTCCCG 99

RESULT 9
HS88A6R/c
LOCUS HS88A6R 160 bp DNA linear PRI 22-OCT-1995
DEFINITION H.sapiens CpG island DNA genomic MseI fragment, clone 88a6, reverse
read cp988a6.r11a.

ACCESSION 263623
VERSION 263623.1 GI:103600
KEYWORDS CpG island; genomic MseI fragment.
SOURCE Homo sapiens.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 160)
AUTHORS Macdonald,M., Hocke,E., Wilkins,P. and Micklem,G.
TITLE Direct Submission
JOURNAL Submitted (16-OCT-1995) The Sanger Centre, Hinxton, Cambridgeshire,
CB10 1HQ, England. E-mail contact: hmquerry@sanger.ac.uk
REFERENCE 2 (bases 1 to 160)
AUTHORS Cross,S.H., Charlton,J.A., Nau,X. and Bird,A.P.
TITLE Purification of CpG islands using a methylated DNA binding column

BASE COUNT 17 a 57 c 46 g 32 t 6 others
ORIGIN

Query Match 100.0%; Score 11; DB 9; Length 160;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTGCTCCCG 11
|||||
DB 89 TTCTGCTCCCG 99

RESULT 9
HS88A6R/c
LOCUS HS88A6R 160 bp DNA linear PRI 22-OCT-1995
DEFINITION H.sapiens CpG island DNA genomic MseI fragment, clone 88a6, reverse
read cp988a6.r11a.

ACCESSION 263623
VERSION 263623.1 GI:103600
KEYWORDS CpG island; genomic MseI fragment.
SOURCE Homo sapiens.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 160)
AUTHORS Macdonald,M., Hocke,E., Wilkins,P. and Micklem,G.
TITLE Direct Submission
JOURNAL Submitted (16-OCT-1995) The Sanger Centre, Hinxton, Cambridgeshire,
CB10 1HQ, England. E-mail contact: hmquerry@sanger.ac.uk
REFERENCE 2 (bases 1 to 160)
AUTHORS Cross,S.H., Charlton,J.A., Nau,X. and Bird,A.P.
TITLE Purification of CpG islands using a methylated DNA binding column